

Application No.: 10/051,902  
Docket No.: BB1163 US DIV

Page 4

### REMARKS

Claims 16-23 are currently pending.

Claims 16-18 have been amended to address the informalities raised on page 2 of the Office Action. No new matter has been added. Withdrawal of the objection to the claims is respectfully requested in view of the above claim clarifications.

Claims 16-23 were rejected under 35 U.S.C. § 112, first paragraph, on the ground that the claims "contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention."

The instant invention concerns an isolated nucleic acid fragment comprising:

(a) a nucleotide sequence encoding a polypeptide having sugar transport protein activity, wherein said polypeptide is at least 66% identical to SEQ ID NO:20;  
or

(b) the full-length complement of the nucleotide sequence of (a).

It is noted that SEQ ID NO:20 is an amino acid sequence encoded by nucleotides 56-1597 of SEQ ID NO:19. There is an ATG codon at position 56-58 and the termination codon is at position 1595-1597 (TGA). The start methionine in SEQ ID NO:20 can be found at position 1.

Also, it is stated on page 22 of the specification that:

The sequence of the entire cDNA insert from clone cepe7.pk0018.g3 is shown in SEQ ID NO:19; the deduced amino acid sequence of this cDNA, which **represents 100% of the of the protein**, is shown in SEQ ID NO:20. A calculation of the percent similarity of the amino acid sequence set forth in SEQ ID NO:20 and the *Beta vulgaris* sequence (using the Clustal algorithm) revealed that the protein encoded by SEQ ID NO:20 is 57% similar to the *Beta vulgaris* sugar transport protein. (Emphasis added.)

Accordingly, SEQ ID NO:20 is the deduced amino acid sequence of a *Beta vulgaris*-like sugar transport protein derived from the nucleotide sequence of SEQ ID NO:19.

Submitted herewith is a copy of Griffith, et al., *Current Opin. Cell Biol.* (1992) 4: 684-695 (Griffith reference), which describes analyses of many transport proteins. An alignment of the amino acid sequences of 34 transporters (including sugar

Application No.: 10/051,902  
Docket No.: BB1163 US DIV

Page 5

transport proteins) is set forth in Figure 2 on page 691. Several categories of highly conserved motifs are discussed starting at the end of the second column on page 687 through page 689. For example, three conserved motifs related to sugar transport activity are the following:

(i) P- E-S-P-R-X-L and P-E-T-K-G-X-X-X-E found at the ends of the sixth and twelfth putative membrane-spanning regions, respectively; and

(ii) (R/K)XGR(R/K) found between the second and third and the eighth and ninth transmembrane helices (Noiraud et al., *The Plant Cell*, 13: 695-705 (March 2001) and Griffith, et al., *Current Opin. Cell Biol.* (1992) 4: 684-695).

Submitted herewith is a copy of Noiraud et al., *The Plant Cell*, 13: 695-705 (March 2001). It is noted that Noiraud et al. was published after the priority date of the instant application and before the filing date of the instant application. Noiraud et al. describe the identification of a mannitol transporter in celery phloem. Figure 1 on page 696 sets forth the nucleotide and deduced amino acid sequences of the celery mannitol transporter (AgMaT1) cDNA. The consensus sequences that are common characteristics in the sugar transporter subfamily were present in AgMaT1.

These same conserved motifs that are common characteristics in sugar transport proteins are also present in SEQ ID NO:20 as shown in Appendix A, submitted herewith. Appendix A is an alignment of

- i) SEQ ID NO:20 (instant invention),
- ii) SEQ ID NO:30 (a sugar beet sequence) also disclosed in the instant application),
- iii) Plant Gene Register PGR97-017 (another sugar beet sequence isolated at the same time), and
- iv) the celery sequence disclosed by Noiraud.

This alignment shows that SEQ ID NO:20 possesses the same conserved motifs that are common characteristics of sugar transport proteins.

Submitted herewith is Appendix B which is a chart setting forth a comparison of the percent identity (and percent divergence in the lower half triangle), among the four sugar transport amino acid sequences aligned in Appendix A.

Another common characteristic of sugar transport proteins is transmembrane helices.

Application No.: 10/051,902  
Docket No.: BB1163 US DIV

Page 6

TMHMM is a software program that allows one to predict the location of transmembrane alpha helices and the location of intervening loop regions. This program will also predict which loops between the helices will be on the inside or outside of the cell or organelle. ( see, e.g., A. Krogh, B. Larsson, G. von Heijne, and E. L. L. Sonnhammer, Predicting transmembrane protein topology with a hidden Markov model: Application to complete genomes. *Journal of Molecular Biology*, 305(3):567-580, January 2001).

SEQ ID NO:20 and the Noiraud et al. celery sequence were analyzed by Applicants using the TMHMM software program. Both sequences were found to possess ten putative transmembrane helices. (Data not shown.)

Parenthetically, it should be noted that Noiraud et al. used the HMMTOP software program (available only to academic institutions) to analyze the celery sequence (Figure 1, page 696). Twelve putative membrane-spanning domains were identified (page 696, bottom of column 1) using HMMTOP.

Accordingly, it is respectfully submitted that the instant specification does possess an adequate written description such that one of skill in the art could reasonably conclude that Applicant was in possession of the claimed invention at the time the instant application was filed.

Withdrawal of the rejection of the claims under 35 USC §112, first paragraph, as lacking adequate written description is respectfully requested.

Claims 16-23 were rejected under 35 U.S.C. § 112, first paragraph, on the ground that the "specification while being enabling for the nucleic acid encoding a polypeptide set forth in (SEQ ID NO:20), does not reasonably provide enablement for any fragments thereof."

It respectfully submitted that the above-discussion with respect to written description is equally apposite to this ground of rejection. It is clear that the same conserved motifs that are common characteristics in sugar transport proteins are also present in SEQ ID NO:20 for all the reasons discussed above and the information set forth in Appendices A and B.

Withdrawal of the rejection of claims 16-23 under 35 USC §112, first paragraph, as lacking an enabling disclosure is respectfully requested.

It is believed that the claims are now in form for allowance which allowance is respectfully requested.

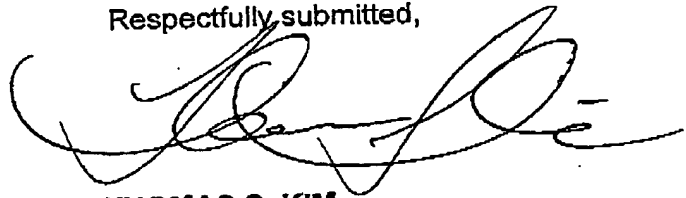
Application No.: 10/051,902  
Docket No.: BB1163 US DIV

Page 7

Submitted herewith are the following: A Petition for a three (3) month extension of time, a Supplemental Information Disclosure Statement, copies of Griffith, Noiraud and the Plant Gene Register references, and Appendices A and B.

Please charge any fees (including the request for a three (3) month extension of time) or credit any overpayment of fees, which are required in connection herewith to Deposit Account No. 04-1928 (E.I. duPont de Nemours and Company).

Respectfully submitted,

**THOMAS S. KIM**

ATTORNEY FOR APPLICANTS

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Dated: 2/27/06

## Appendix A (page 1 of 3)

N.....A..CA..LASN..S..LGVD..GV..SG							Consensus #1
1	10	20	30	40	50	60	SEQ ID NO20.pro
1	10	20	30	40	50	60	SEQ ID NO30 (GI 1778093).pro
1	10	20	30	40	50	60	U64903 (GI 1778094).pro
1	10	20	30	40	50	60	AF215837 (GI 12004315).pro
1	10	20	30	40	50	60	Consensus #1
A..Y..K..D...D...Q.....GI...Y..L..GS.....RTSH..IGRR..T..V..A...IV..G... (R/KXGR(R/K							Consensus #1
45	70	80	90	100	110	120	SEQ ID NO20.pro
61	70	80	90	100	110	120	SEQ ID NO30 (GI 1778093).pro
61	70	80	90	100	110	120	U64903 (GI 1778094).pro
48	70	80	90	100	110	120	AF215837 (GI 12004315).pro
MG.A.N....LM.GRPV..Q.GVG...NIAPVYTA...P...SRGPVT..PPEVFIN..G..LLGY							Consensus #1
105	130	140	150	160	170	180	SEQ ID NO20.pro
121	130	140	150	160	170	180	SEQ ID NO30 (GI 1778093).pro
121	130	140	150	160	170	180	U64903 (GI 1778094).pro
108	130	140	150	160	170	180	AF215837 (GI 12004315).pro
.SN..AP....P...L..WR..ML..IGA..PS...LA...V...NPESPRML...GRL...A...VL...S							Consensus #1
165	190	200	210	220	230	240	SEQ ID NO20.pro
181	190	200	210	220	230	240	SEQ ID NO30 (GI 1778093).pro
181	190	200	210	220	230	240	U64903 (GI 1778094).pro
168	190	200	210	220	230	240	AF215837 (GI 12004315).pro

PESPRWL or PESPRXL

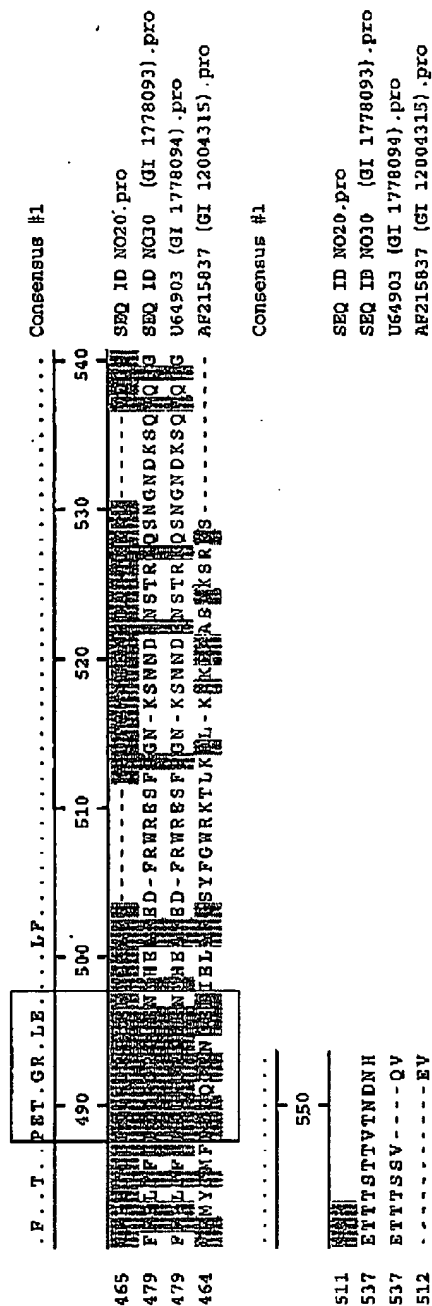
## Appendix A (page 2 of 3)

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(R/K)XGR(R/K)

## Appendix A (page 3 of 3)

PETQGRXXE – SEQ ID NO20 has an R in place of the Q (similar to sugar beet sequences)



The boxed residues correspond to the sequences conserved in the sugar transporter subfamily of the major facilitator superfamily (MFS).

Shade (with black at 40% fill) residues that match SEQ ID NO20 (corn) exactly.

Consensus #1: When all match the residue of the Consensus show the residue of the Consensus, otherwise show ''.

## Appendix B

## Percent Identity

	1	2	3	4	
1	■	56.5	56.5	52.4	1
2	59.0	■	99.3	61.6	2
3	59.0	0.7	■	61.6	3
4	63.9	50.5	50.1	■	4
	1	2	3	4	

Divergence

SEQ ID NO20 (corn)  
 SEQ ID NO30 (NCBI GI 1778093) (sugar beet)  
 U64903 (NCBI GI 1778094) (sugar beet)  
 AF215837 (NCBI GI 12004315) (celery)